

FIG. 1-1

ESX ORF DNA Sequence (1 to 1116) -> 1-phase Translation
 DNA sequence 1116 b.p. ATGGCTGCAACC ... agtcggaactga linear

371 Amino acids
 MW: 41428 Dalton

1/1	31/11	61/21
ATG GCT GCA ACC TGT GAG ATT AGC AAC ATT TTT AGC AAC TAC TTC AGT GCG ATG TAC AGC TCG GAG GAC TCC ACC CTG GCC TCT GTT CCC		
Met ala ala thr cys glu ile ser asn ile phe ser asn tyr phe ser ala met tyr ser ser glu asp ser thr leu ala ser val pro		
91/31	121/41	151/51
CCT GCT GCC ACC TTT GGG GCC GAT GAC TTG GTA CTG ACC CTG AGC AAC CCC CAG ATG TCA TTG GAG GGT ACA GAG AAG GCC AGC TGG TTG		
pro ala ala thr phe gly ala asp asp leu val leu thr leu ser asn pro gln met ser leu glu gly thr glu lys ala ser trp leu		
181/61	211/71	241/81
GGG GAA CAG CCC CAG TTC TGG TCG AAG ACG CAG GTT CTG GAC TGG ATC AGC TAC CAA GTG GAG AAG AAC AAG TAC GAC GCA AGC GCC ATT		
gly glu gln pro gln phe trp ser lys thr gln val leu asp trp ile ser tyr gln val glu lys asn lys tyr asp ala ser ala ile		
271/91	301/101	331/111
GAC TTC TCA CGA TGT GAC ATG GAT GGC GCC ACC CTC TGC AAT TGT GCC CTT GAG GAG CTG CGT CTG GTC TTT GGG CCT CTG GGG GAC CAA		
asp phe ser arg cys asp met asp gly ala thr leu cys asn cys ala leu glu glu leu arg leu val phe gly pro leu gly asp gln		
361/121	391/131	421/141
CTC CAT GCC CAG CTG CGA GAC CTC ACT TCC AGC TCT TCT GAT GAG CTC AGT TGG ATC ATT GAG CTG CTG GAG AAG GAT GGC ATG GCC TTC		
lau his ala gln leu arg asp leu thr ser ser ser asp glu leu ser trp ile ile glu leu leu glu lys asp gly met ala phe		
451/151	481/161	511/171
CAG GAG GCC CTA GAC CCA GGG CCC TTT GAC CAG GGC AGC CCC TTT GCC CAG GAG CTG CTG GAC GAC GGT CAG CAA GCC AGC CCC TAC CAC		
gln glu ala leu asp pro gly pro phe asp gln gly ser pro phe ala gln glu leu leu asp asp gly gln ala ser pro tyr his		
541/181	571/191	601/201
CCC GGC AGC TGT GGC GCA GGA GCC CCC TCC CCT GGC AGC TCT GAC GTC TCC ACC GCA GGG ACT GGT GCT TCT CGG AGC TCC CAC TCC TCA		
pro gly ser cys gly ala gly ala pro ser pro gly ser ser asp val ser thr ala gly thr gly ala ser arg ser ser his ser ser		
631/211	661/221	691/231
GAC TCC GGT GGA AGT GAC GTG GAC CTG GAT CCC ACT GAT GGC AAG CTC TTC CCC AGC GAT GGT TTT CGT GAC TGC AAG AAG GGG GAT CCC		
asp ser gly gly ser asp val asp leu asp pro thr asp gly lys leu phe pro ser asp gly phe arg asp cys lys lys gly asp pro		



FIG. 1-2

811/271 841/281 871/291
AGA GGC ACC CAC CTG TGG GAG TTC ATC CGG GAC ATC CTC ATC CAC CCG GAG CTC AAC GAG GGC CTC ATG AAG TGG GAG AAT CGG CAT GAA
arg gly thr his leu trp glu phe ile arg asp ile leu ile his pro glu leu asn glu gly leu met lys trp glu asn arg his glu
901/301 931/311 961/321
GGC GTC TTC aag TTC CTG CGC TCC GAG GCT GTG GCC CAA CTA TGG GGC CAA AAG AAA AAG AAC AGC AAC ATG ACC TAC GAG AAG CTG AGC
gly val phe lys phe leu arg ser glu ala val ala gln leu trp gly gln lys lys asn ser asn met thr tyr glu lys leu ser
991/331 1021/341 1051/351
CGG GCC ATG AGG TAC TAC AAA CGG GAG ATC CTG GAA CGG GTG GAT GGC CGG CGA CTC GTC TAC AAG TTT GGC AAA AAC TCA AGC GGC
arg ala met arg tyr tyr tyr lys arg glu ile leu glu arg val asp gly arg arg leu val tyr lys phe gly lys asn ser ser gly
1081/361 1111/371
TGG AAG GAG GAA GAG GTT CTC CAG AGT CGG AAC TGA
trp lys glu glu glu val leu gln ser arg asn OPA



FIG. 2a

MAATCEISNIFSNYFSAMYSSDSTLASVPPAATFGADDLVLTLSNPQMSLEG 53

TEKASWLGEQ**PQFWSKTQVLDWISYQVEKNKYDASAIIDFSRCDMDGATLC**NCA 106

LEELRLVFGPLGDQLHAQLRDLTSSSSDELSWIIELLEKDGMAFQEALDPGPF 159

DQGSPFAQELLDDGQQASPYHPGSCGAG**APSPGSSDVSTAGTGASRSSHSSDS** 212

GGSDVDLDPTDGKLFPSDGFRDCKKGDPKHGKRKRGRPRKLSKEYWDCLEGKK 265

SKHAPRG**TLWEFIRDILIHPELNEGLMKWENRHEGVFKFLRSEAVAQLWGQK** 318

KKNSNMTYEKLSRAMRYYYKREILERVDGRRLVYKFGKNSSGWKEEEVLQSRN 371

FIG. 2a

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FIG. 2a



FIG. 2b

Consensus[†]: P W V W W E G LC
ESX (64-103): PQFWSKTQVLDWISYQVEKNKYDASAI DFSRCMDGATLC
P+ W++T V DW+ + V N++ +DF + M+GA LC
ETS-1 (69-106): PRQWTETHVRDWMWAV--NEFSLKGVDFQKFCMNGAALC

FIG. 2c

ESX (188-238): APSGGSSDVSTAGTASRSSHSSDGGSDVDLPTDGLFPDGFDRDCKKG
APS S S++ + S SS SS S SD + + L PS F G
SOX4 (370-420): APSSAPSHASSASSSSSSSSSSDDEFEDDLLDLPSSNFESMSLG

FIG. 2d

Consensus[†]: LWQFLL LL D I W FK VAR WG K P MNY KLSR LRYYY I K G R Y F
* * * * *
ESX (274-354): HLWEIFIRDLIHPELNEGLMKWENRHEGVFKFLRSEAVAQLWGQKKNSNMTYEKLSRAMRYYYKKREILERVDRRLVYKF
+LWEF+ +L +KW R +G+FK + S+AV++LWG+ K +M YE + RA+RYYY+R IL +V+G+RLVY+F
ELF-1 (209-289): YLWFEFLALLQDKATCPKYIKWTQREKGIFKLVDKAVSRNLWGKHKNKPD MN YETMGRALRYYYQRGILAKVEGQRLVYQF

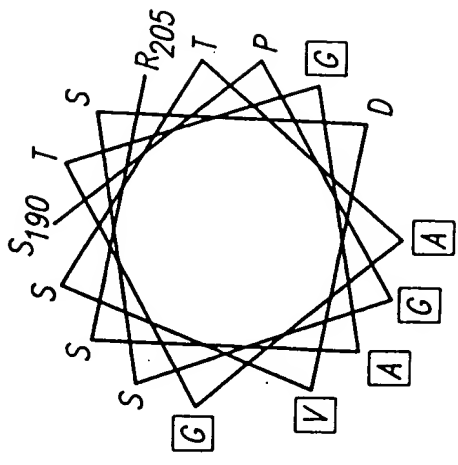




FIG. 2e

MAATCEISNIFSNYFSAMYSSDSTLASVPPAATFGADDLVLTLSNPQMSLEG	53
TEKASWLGEQPQFWSKTQVLDWISYQVEKNKYDASAIIDFSRCDMDGATLCNCA	106
LEELRLVFGPLGDQLHAQLRDLTSSSSDELSWIELLEKDGMAFQEALDPGPF	159
.	
DQGSPFAQELLDDGQASPYHPGSCGAGAPSPGSSDVSTAGTGASRSSHSSDS	212
GGSDVDLDPTDGKLFPSDGFRCCKGDPKHGKRKRGRPRKLSKEYWDCLEGKK	265
SKHAPRGTHLWEFIRDILIHPELNEGLMKWENRHEGVFKFLRSEAVAQLWGQK	318
KKNSNMTYEKLSRAMRYYYKREILERVGDGRRRLVYKFGKNSSGWKEEEVLQSRN	371

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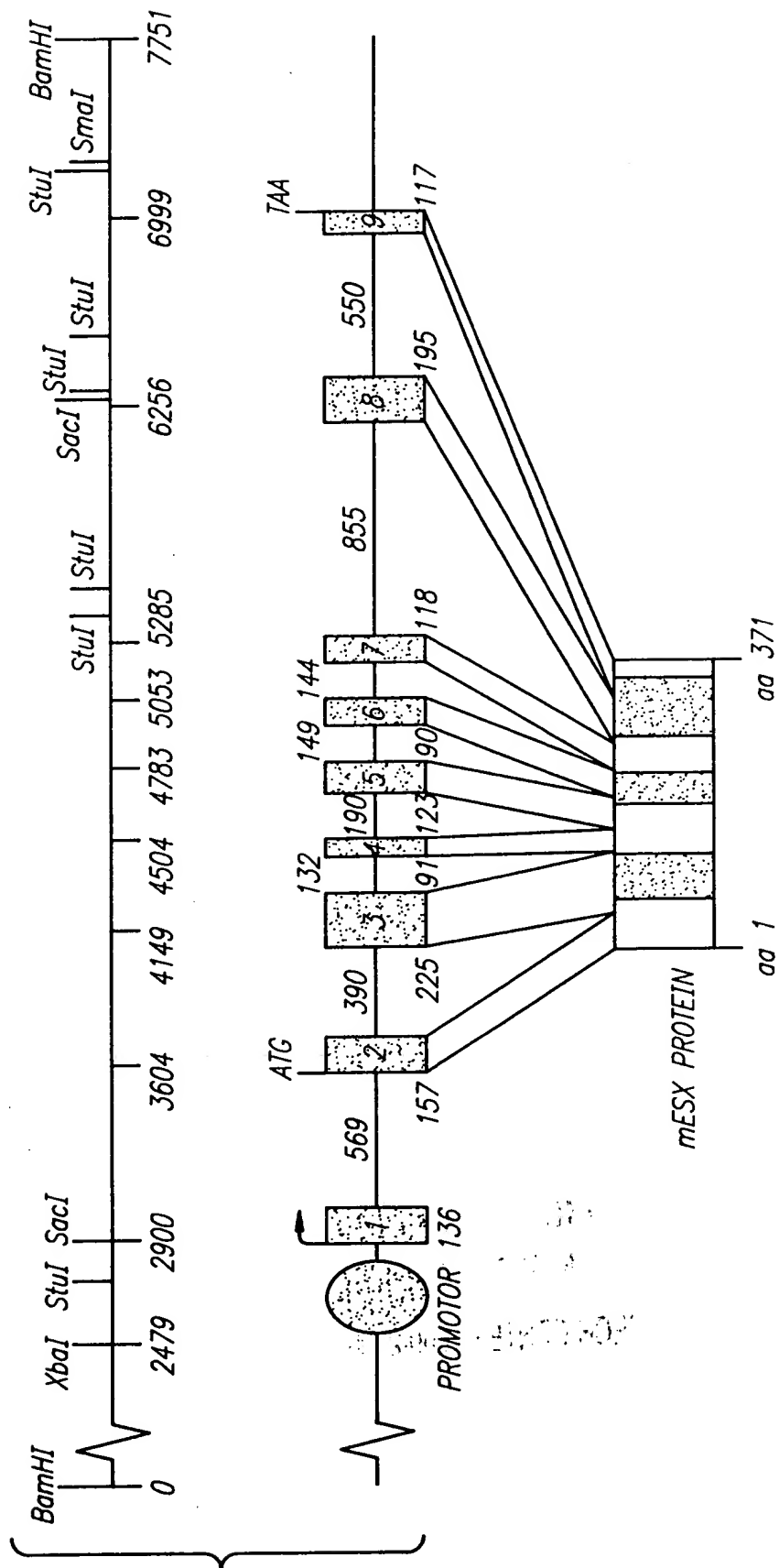


FIG. 3



FIG. 4-1

1/1 31/11
ATG GCT GCA ACC TGT GAG ATT AGC AAC ATT TTT AGC AAC TAC TTC AGT GCG ATG TAC AGC
Met ala ala thr cys glu ile ser asn ile phe ser asn tyr phe ser ala met tyr ser
61/21 91/31
TCG GAG GAC TCC ACC CTG GCC TCT GTT CCC CCT GCT GCC ACC TTT GGG GCC GAT GAC TTG
ser glu asp ser thr leu ala ser val pro pro ala ala thr phe gly ala asp asp leu
121/41 151/51 E2 ▼ E3
GTA CTG ACC CTG AGC AAC CCC CAG ATG TCA TTG GAG GGT ACA GAG AAG GCC AGC TGG TTG
val leu thr leu ser asn pro gln met ser leu glu gly thr glu lys ala ser trp leu
181/61 211/71
GGG GAA CAG CCC CAG TTC TGG TCG AAG ACG CAG GTT CTG GAC TGG ATC AGC TAC CAA GTG
gly glu gln pro gln phe trp ser lys thr gln val leu asp trp ile ser tyr gln val
241/81 271/91
GAG AAG AAC AAG TAC GAC GCA AGC GCC ATT GAC TTC TCA CGA TGT GAC ATG GAT GGC GCC
glu lys asn lys tyr asp ala ser ala ile asp phe ser arg cys asp met asp gly ala
301/101 331/111
ACC CTC TGC AAT TGT GCC CTT GAG GAG CTG CGT CTG GTC TTT GGG CCT CTG GGG GAC CAA
thr leu cys asn cys ala leu glu glu leu arg leu val phe gly pro leu gly asp gln
361/121 E3 ▼ E4 391/131
CTC CAT GCC CAG CTG CGA GAC CTC ACT TCC AGC TCT TCT GAT GAG CTC AGT TGG ATC ATT
leu his ala gln leu arg asp leu thr ser ser ser asp glu leu ser trp ile ile
421/141 E4 ▼ E5 451/151
GAG CTG CTG GAG AAG GAT GGC ATG GCC TTC CAG GAG GCC CTA GAC CCA GGG CCC TTT GAC
glu leu leu glu lys asp gly met ala phe gln glu ala leu asp pro gly pro phe asp

FIG. 4-2

481/161 511/171
CAG GGC AGC CCC TTT GCC CAG GAG CTG CTG GAC GAC GGT CAG CAA GCC AGC CCC TAC CAC
gln gly ser pro phe ala gln glu leu asp asp gly gln ala ser pro tyr his
541/181 571/191
CCC GGC AGC TGT GGC GCA GGA GCC Ccc TCC CCT GGC AGC TCT GAC GTC TCC ACC GCA GGG
pro gly ser cys gly ala gly ala pro ser pro gly ser ser asp val ser thr ala gly
601/201 631/211
ACT GGT GCT TCT CGG AGC TCC CAC TCC TCA GAC TCC GGT GGA AGT GAC GTG GAC CTG GAT
thr gly ala ser arg ser his ser ser asp ser gly gly ser asp val asp leu asp
661/221 691/231
CCC ACT GAT GGC AAG CTC TTC CCC AGC GAT GGT TTT CGT GAC TGC AAG AAG GGG GAT CCC
pro thr asp gly lys leu phe pro ser asp gly phe arg asp cys lys lys gly asp pro
721/241 751/251
AAG CAC GGC AAG CGG AAA CGA GGC CGG CCC CGA AAG CTG AGC AAA GAG TAC TGG GAC TGT
lys his gly lys arg lys arg gly arg pro arg lys leu ser lys glu tyr trp asp cys
781/261 811/271
CTC GAG GGC AAG AGC AAG CAC GCG CCC AGA GGC ACC CAC CTG TGG GAG TTC ATC cGG
leu glu gly lys lys ser lys his ala pro arg gly thr his leu trp glu phe ile arg
841/281 871/291
GAC ATC CTC ATC CAC CCG GAG CTC AAC GAG GGC CTC ATG AAG TGG GAG AAT CGG CAT GAA
asp ile leu ile his pro glu leu asn glu gly leu met lys trp glu asn arg his glu
901/301 931/311
GGC GTC TTC aag TTC CTG CGC TCC GAG GCT GTG GCC CAA CTA TGG GGC CAA AAG AAA AAG
gly val phe lys phe leu arg ser glu ala val ala gln leu trp gly gln lys lys lys



FIG. 4-3

961/321
AAC AGC AAC ATG ACC TAC GAG AAG CTG AGC CGG GCC ATG AGG TAC TAC TAC AAA CGG GAG
asn ser asn met thr tyr glu lys leu ser arg ala met arg tyr tyr tyr lys arg glu
1021/341
ATC CTG GAA CGG GTG GAT GGC CGG CGA CTC GTC TAC AAG TTT GGC AAA AAC TCA AGC GGC
ile leu glu arg val asp gly arg arg leu val tyr lys phe gly lys asn ser ser gly
1081/361
TGG AAG GAG GAA GAG GTT CTC CAG AGT CGG AAC TGA
trp lys glu glu glu val leu gln ser arg asn OPA

991/331 E8 E9



FIG. 5-2

E_8/E_9
↓

mESX 300	EGVFKFLRSEAVAQLWGQKKKNSNMTYEKLSRAMRYYYKREILERV DGR	349
hESX 300	EGVFKFLRSEAVAQLWGQKKKNSNMTYEKLSRAMRYYYKREILERV DGR	349

mESX 350	LVYKFGKNSSGWKEEEVGESRN	371
hESX 350	LVYKFGKNSSGWKEEVLQSRN	371





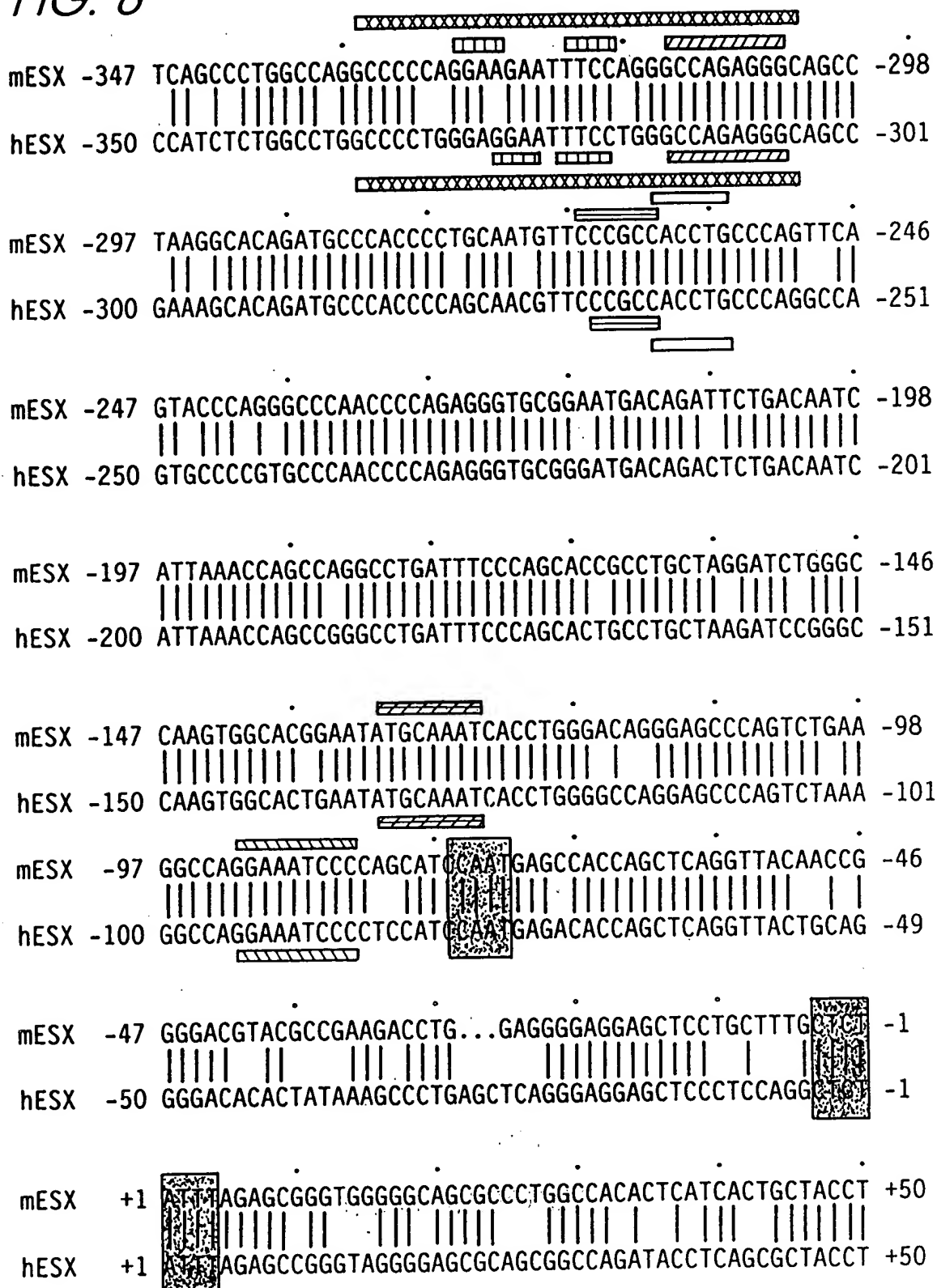
-  POINTED/A-Region
-  Serine-Rich Box
-  Nuclear Targeting Sequence
-  ETS-DNA Binding Domain

FIG. 6



Ets	extended palindrome	USF
AP-2	SPI/GC box	Oct
NF-kB	CCAAT box & Inr element	

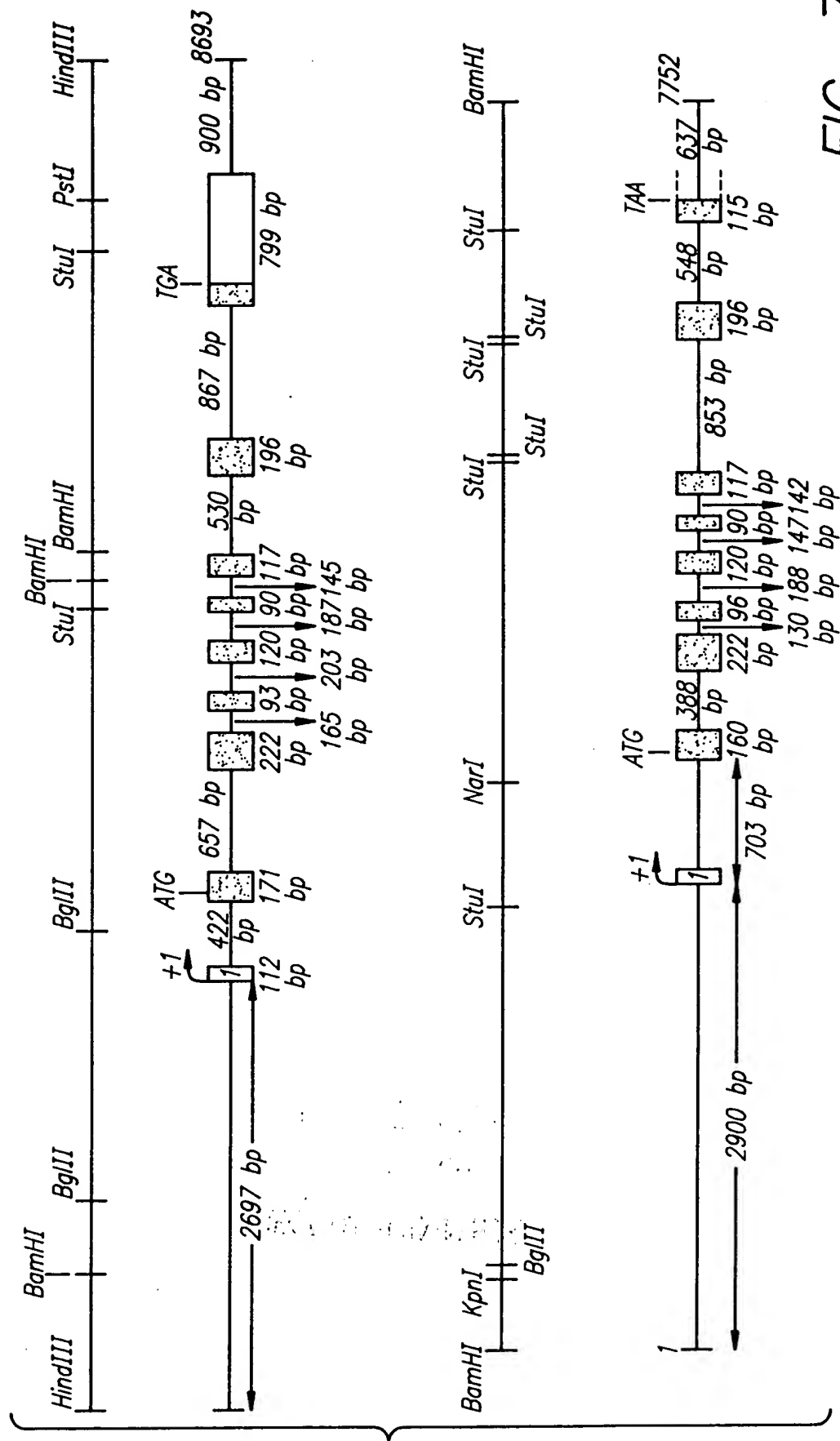
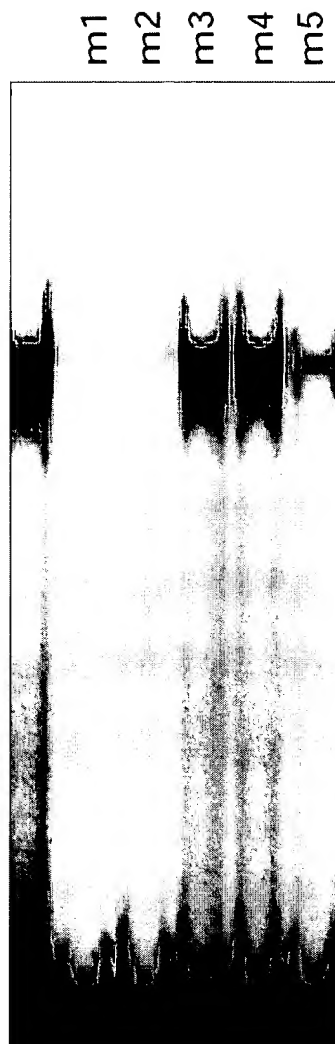


FIG. 7



WT 5' GGAGGAGGGCTGCTTGAGGAAGTATAAGAAT 3'
m1 5' -----TA----- 3'
m2 5' -----C----- 3'
m3 5' -----AG----- 3'
m4 5' -----CC----- 3'
m5 5' -----C----- 3'

Fig. 8A

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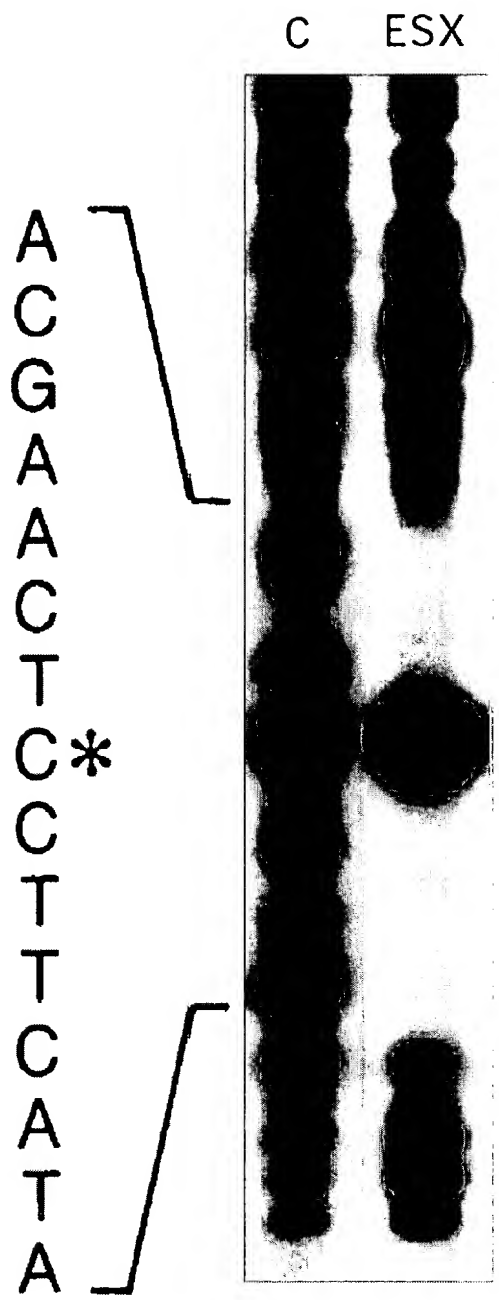


Fig. 8B

FIG. 8B

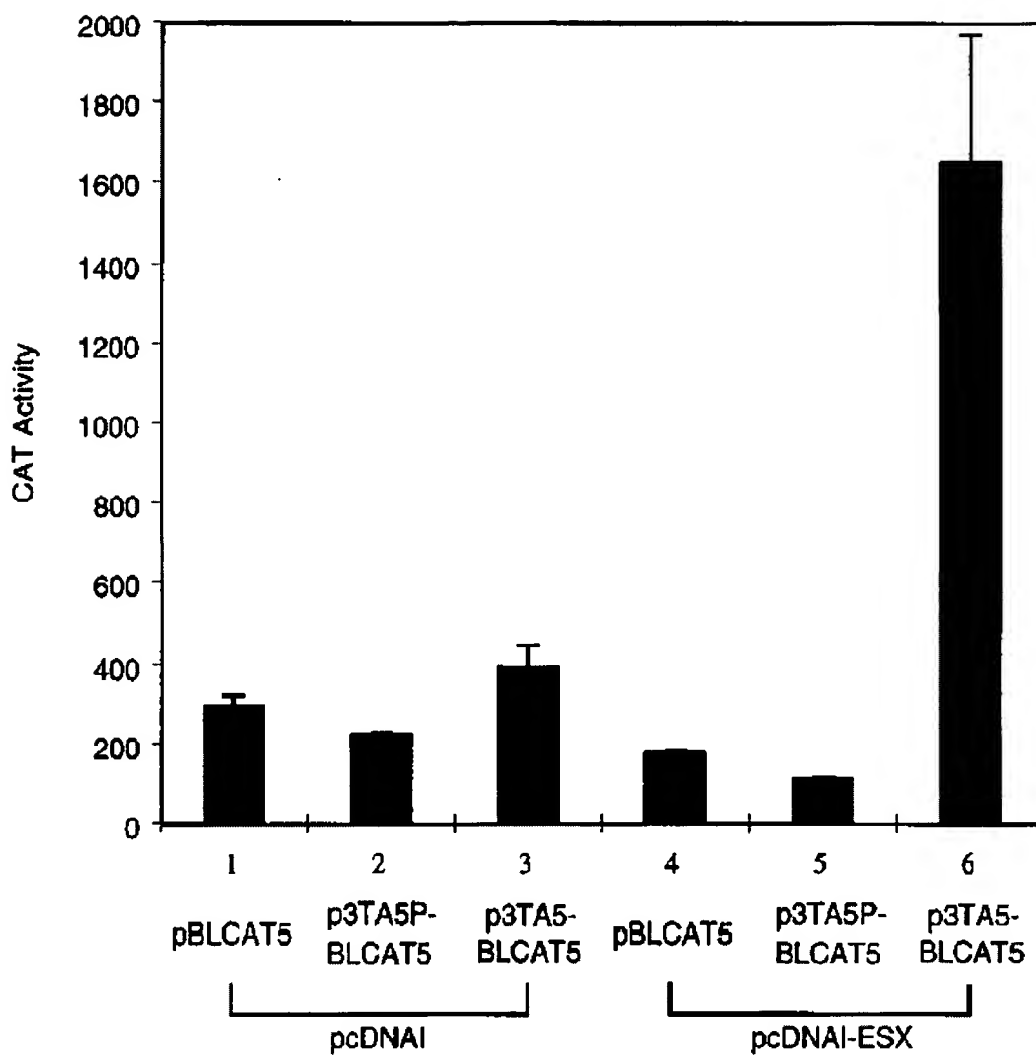


Fig. 8C

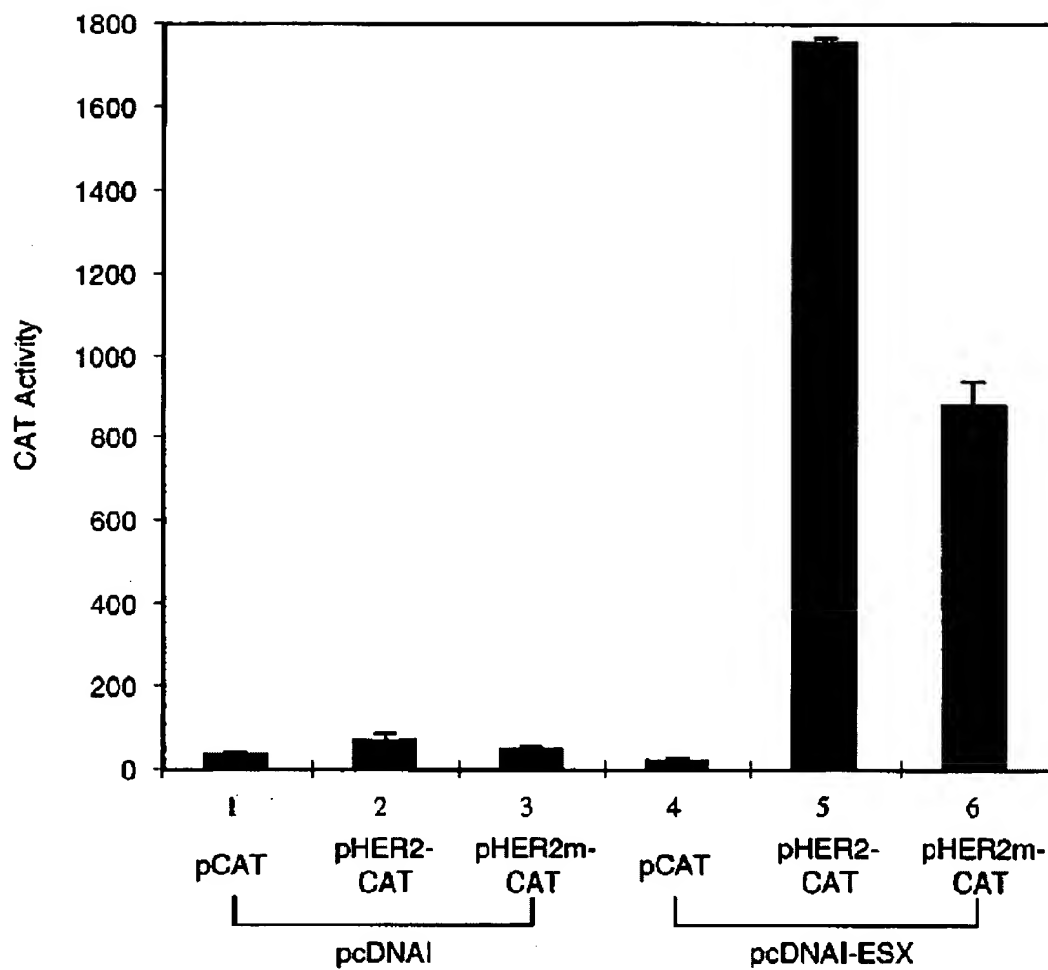


Fig. 8D

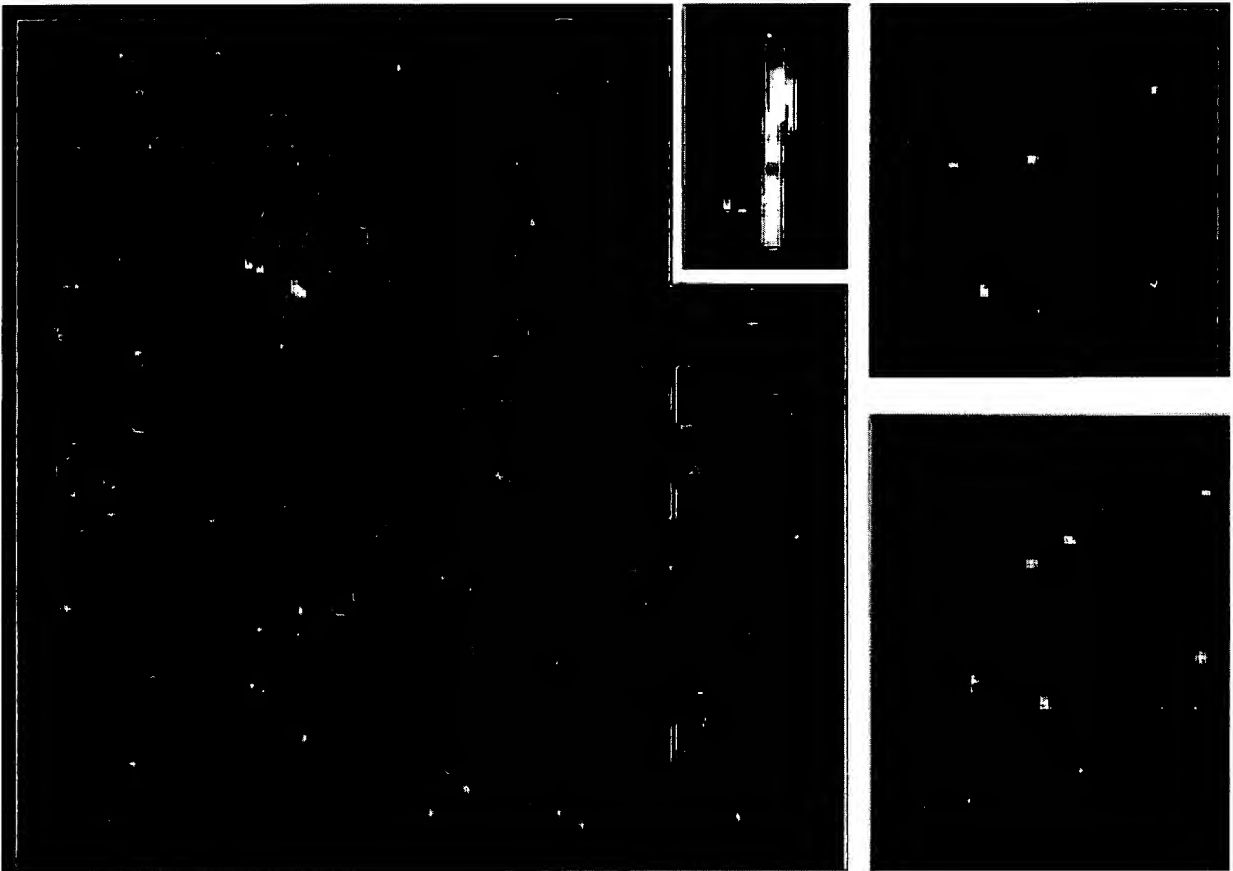


Fig. 8E

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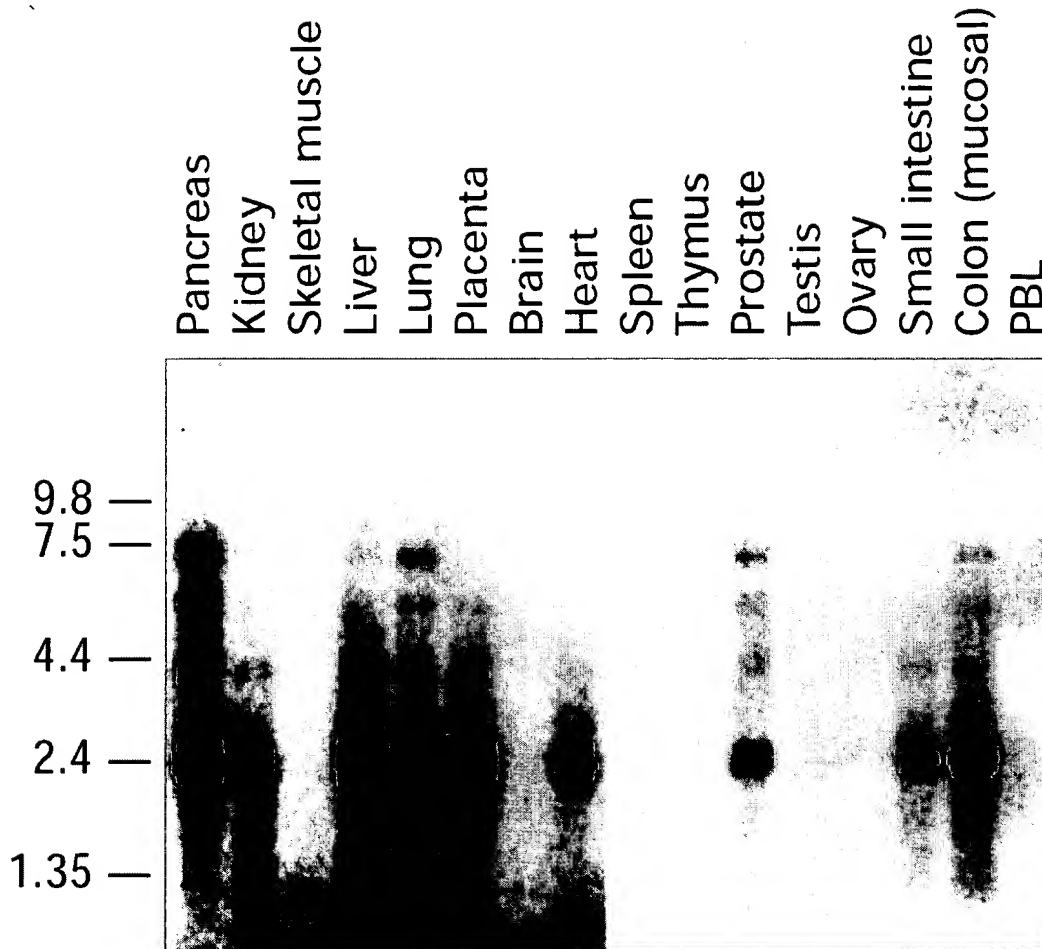


Fig. 9A

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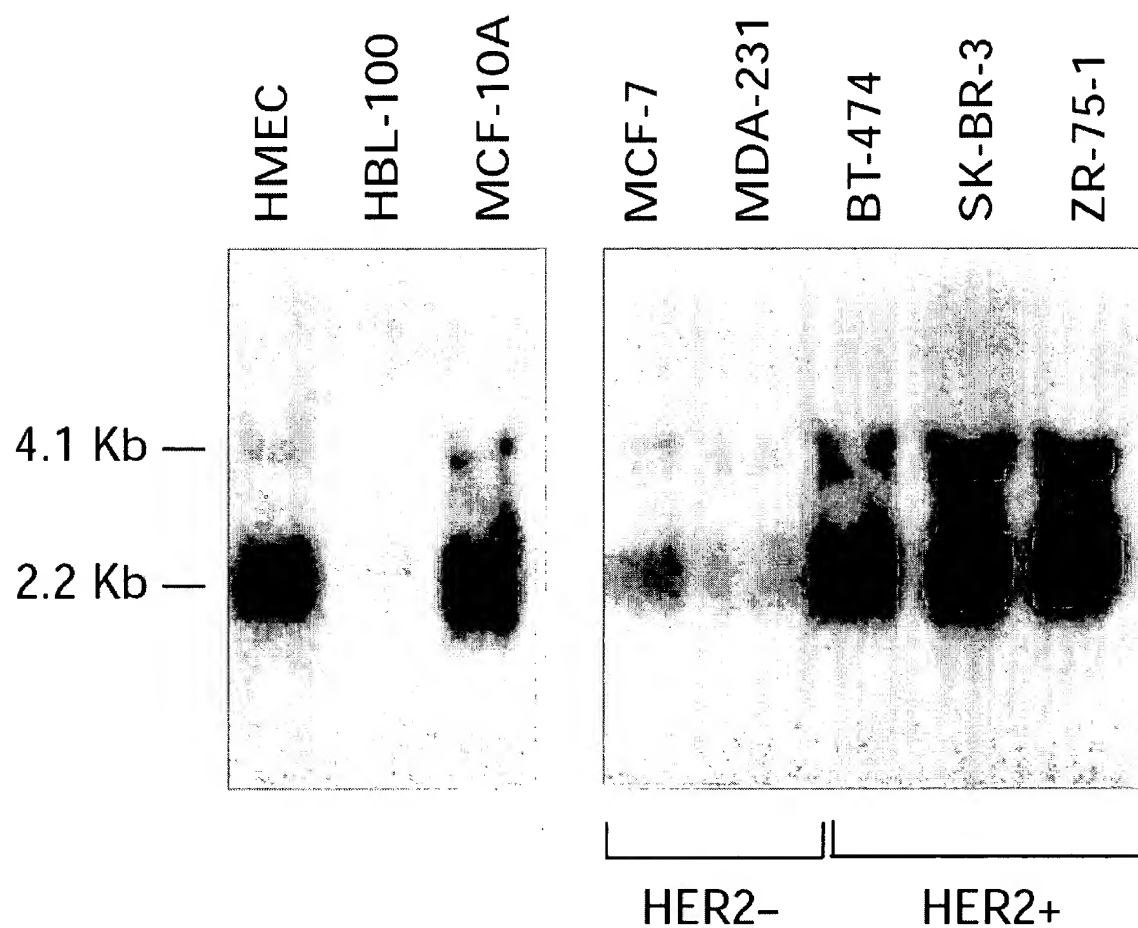
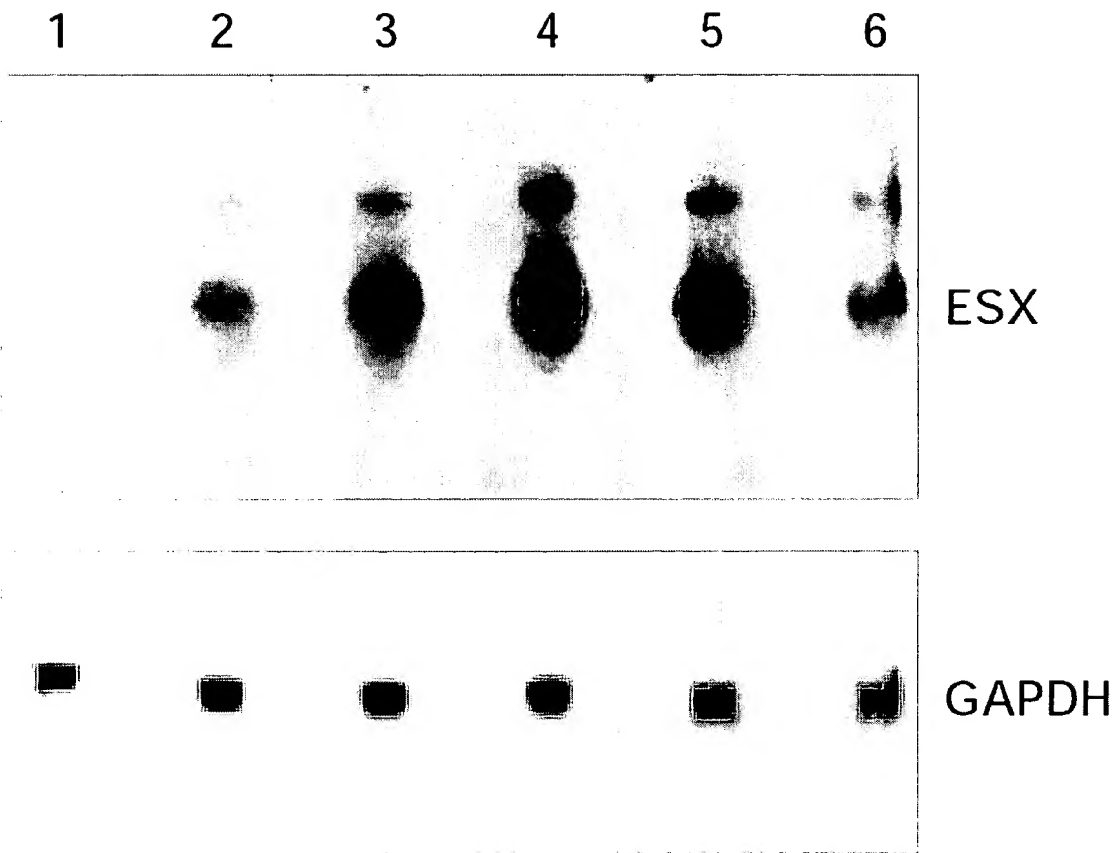


Fig. 9B

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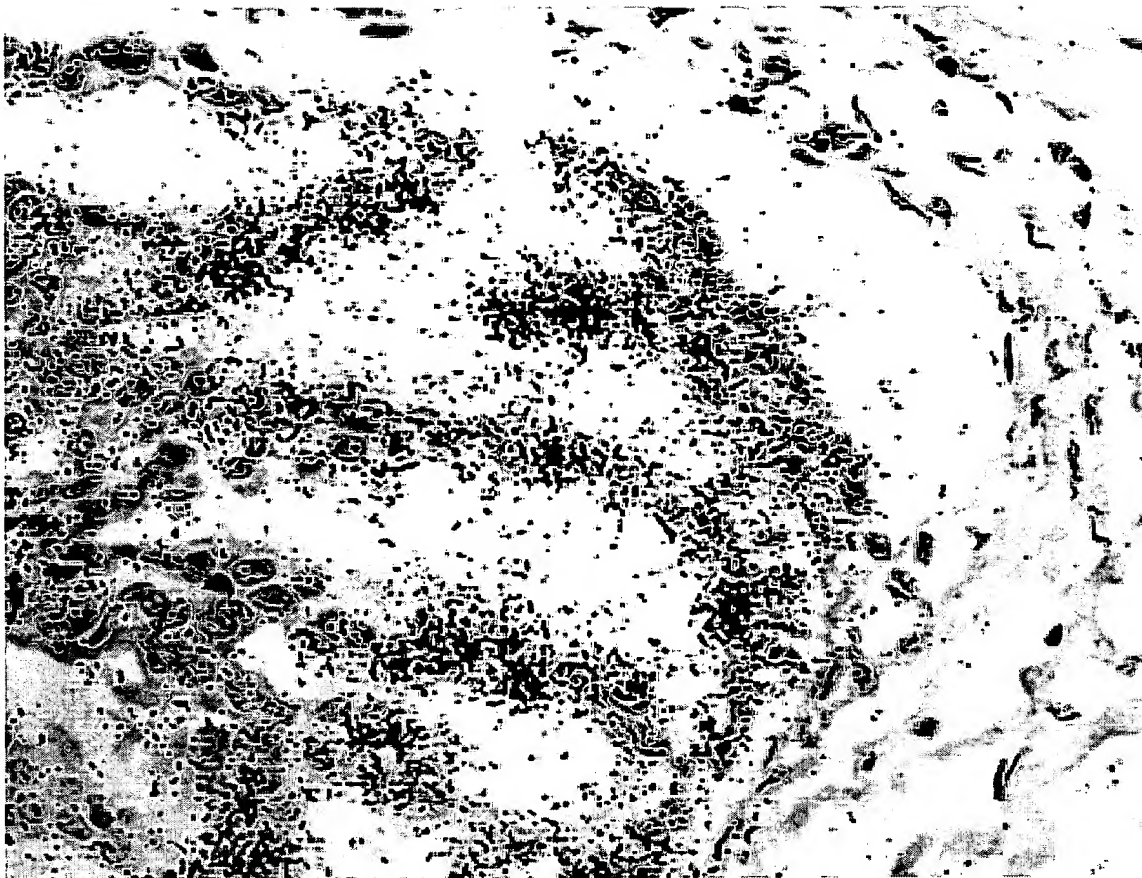


Fig. 10A

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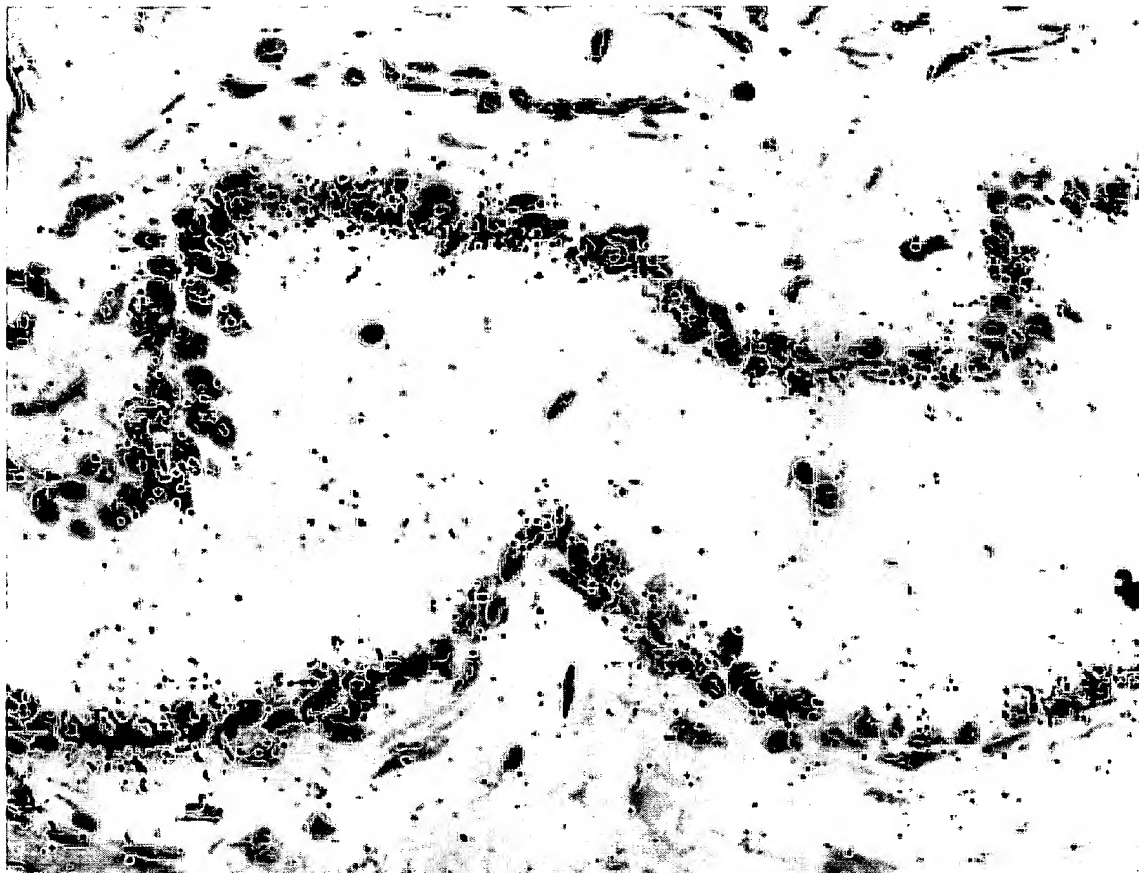


Fig. 10B

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10/10/02
10/10/02